SEQUENCE LISTING

<110> Junghans, Richard P.

<120> Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti
gens

<130> 003

<140> 10/066,773
<141> 2001-10-12

<150> 60/250,089
<151> 2000-11-30

<160> 19

<170> PatentIn version 3.1

<210> 1
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<213> Homo sapiens and Mus sp.

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<221> CDS
<222> (2428)..(3759)
<223> Chimeric IgTCR sequence contained in retroviral vector. Retrovir
al vector sequence (non-coding regions) are incidental to the inv
ention. The translated (coding region) is relevant to the invent
ion. (pertinent to Figure 3.)

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Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
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Cys Lys Ala Ser Gln Asp Val Gly Thr Ser Val Ala Trp Tyr Gln Gln
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aag cca ggt aag gct cca aag ctg ctg atc tac tgg aca tcc acc cgg      2646
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg
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cac act ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt acc gac      2694
His Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
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ttc acc ttc acc atc agc agc ctc cag cca gag gac atc gcc acc tac      2742
Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr
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Tyr Cys Gln Gln Tyr Ser Leu Tyr Arg Ser Phe Gly Gln Gly Thr Lys
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Val Glu Ile Lys Arg Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly
            125                    130                    135

ggc tca gga tcg gag gtc caa ctg gtg gag agc ggt gga ggt gtt gtg    2886
Gly Ser Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val
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caa cct ggc cgg tcc ctg cgc ctg tcc tgc tcc gca tct ggc ttc gat    2934
Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp
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Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
170                    175                    180                    185

ctt gag tgg att gga gaa att cat cca gat agc agt acg att aac tat    3030
Leu Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr Ile Asn Tyr
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gcg ccg tct cta aag gat aga ttt aca ata tcg cga gac aac gcc aag    3078
Ala Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
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aac aca ttg ttc ctg caa atg gac agc ctg aga ccc gaa gac acc ggg    3126
Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly
            220                    225                    230

gtc tat ttt tgt gca agc ctt tac ttc ggc ttc ccc tgg ttt gct tat    3174
Val Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp Phe Ala Tyr
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tgg ggc caa ggg acc ccg gtc acc gtc tcc agt gct aag ccc acc acg    3222
Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Ala Lys Pro Thr Thr
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acg cca gcg ccg cga cca cca aca ccg gcg ccc acc atc gcg tcg cag    3270
Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
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ccc ctg tcc ctg cgc cca gag gcg gct cgg cca gcg gcg ggg ggc gca    3318
Pro Leu Ser Leu Arg Pro Glu Ala Ala Arg Pro Ala Ala Gly Gly Ala
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gtg cac acg agg ggg ctg gac ttc gcc ctg gat ccc aaa ctc tgc tac    3366
Val His Thr Arg Gly Leu Asp Phe Ala Leu Asp Pro Lys Leu Cys Tyr
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ttc ctg aga gtg aag ttc agc agg agc gca gag ccc ccc gcg tac cag      3462
Phe Leu Arg Val Lys Phe Ser Arg Ser Ala Glu Pro Pro Ala Tyr Gln
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cag ggc cag aac cag ctc tat aac gag ctc aat cta gga cga aga gag      3510
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gag tac gat gtt ttg gac aag aga cgt ggc cgg gac cct gag atg ggg      3558
Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
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gga aag ccg aga agg aag aac cct cag gaa ggc ctg tac aat gaa ctg      3606
Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
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cag aaa gat aag atg gcg gag gcc tac agt gag att ggg atg aaa ggc      3654
Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
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gag cgc cgg agg ggc aag ggg cac gat ggc ctt tac cag ggt ctc agt      3702
Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
410                 415                 420                 425

aca gcc acc aag gac acc tac gac gcc ctt cac atg cag gcc ctg ccc      3750
Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
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Pro Arg


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tatagagtac gagccataga taaaataaaa gattttattt agtctccaga aaaagggggg   3919

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<213>  Homo sapiens and Mus sp.

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            20              25              30

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val
        35              40              45

Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
    50              55              60
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Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg
65   70   75   80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
                 85   90   95

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu
            100   105   110

Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly
        115   120   125

Ser Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Glu Val Gln
    130   135   140

Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg
145   150   155   160

Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe Thr Thr Tyr Trp Met Ser
                165   170   175

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile
            180   185   190

His Pro Asp Ser Ser Thr Ile Asn Tyr Ala Pro Ser Leu Lys Asp Arg
            195   200   205

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Phe Leu Gln Met
    210   215   220

Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala Ser Leu
225   230   235   240

Tyr Phe Gly Phe Pro Trp Phe Ala Tyr Trp Gly Gln Gly Thr Pro Val
                245   250   255

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Thr Val Ser Ser Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro
        260             265             270

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
        275             280             285

Ala Ala Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
    290             295             300

Phe Ala Leu Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu Phe
305             310             315             320

Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe Ser
            325             330             335

Arg Ser Ala Glu Pro Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr
            340             345             350

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
        355             360             365

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
    370             375             380

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
385             390             395             400

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
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His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
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Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
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<223>   MB3.6 Heavy chain V region, plus leader


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      Met Asn Phe Gly Phe Ser Leu Ile Phe Leu Val Leu Val Leu Lys
      1               5                   10                  15

ggt gtc cag tgt gaa gtg gtg gtg gtg gag tct ggg gga ggc ttc gtg        98
Gly Val Gln Cys Glu Val Val Val Val Glu Ser Gly Gly Gly Phe Val
                20                  25                  30

aag cct gga ggg tcc ctg aaa ctc tcc tgt gca gcc gct gga ttc act       146
Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ala Gly Phe Thr
            35                  40                  45

ttc agt aga tat gcc atg tct tgg gtt cgc cag act ccg gag aag agg       194
Phe Ser Arg Tyr Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg
        50                  55                  60

ctg gag tgg gtc gca acc ata agt agt ggt ggt agt cac acc tac tat       242
Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser His Thr Tyr Tyr
    65                  70                  75

cca gac agt gtg aag ggg cga ttc acc atc tcc aga gac aat gcc aag       290
Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
80                  85                  90                  95

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Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala
                100                 105                 110

ata tat tac tgt gca aga ccg ggt tac gac agg ggg gcc tgg ttt ttc       386
Ile Tyr Tyr Cys Ala Arg Pro Gly Tyr Asp Arg Gly Ala Trp Phe Phe
            115                 120                 125

gat gtc tgg ggc gca ggg acc acg gtc acc gtc tcc tca ggtaagtgtg        435
Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
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Val Gln Cys Glu Val Val Val Val Glu Ser Gly Gly Gly Phe Val Lys
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Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ala Gly Phe Thr Phe
            35   40   45

Ser Arg Tyr Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu
        50   55   60

Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser His Thr Tyr Tyr Pro
65   70   75   80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
                85   90   95

Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Ile
                100   105   110

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        115   120   125

Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
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<220>
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ttt tgg att tca gcc tcc aga ggt gat att gtg cta act cag tct cca       99
Phe Trp Ile Ser Ala Ser Arg Gly Asp Ile Val Leu Thr Gln Ser Pro
            15              20                  25

gcc acc ctg tct gtg act cca gga gat agc gtc agt ctt tcc tgc agg      147
Ala Thr Leu Ser Val Thr Pro Gly Asp Ser Val Ser Leu Ser Cys Arg
    30                  35                  40

gcc agc caa att att agc aac aac cta cac tgg tat caa caa aaa tca      195
Ala Ser Gln Ile Ile Ser Asn Asn Leu His Trp Tyr Gln Gln Lys Ser
45                  50                  55                  60

cat gag tct cca agg ctt ctc atc aag tat gct tcc cag tcc atc tct      243
His Glu Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Gln Ser Ile Ser
            65                  70                  75

ggg atc ccc tcc agg ttc agt ggc agt gga tca ggg aca gat ttc act      291
Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
            80                  85                  90

ctc agt atc aac agt gtg gag act gaa gat ttt gga atg tat ttc tgt      339
Leu Ser Ile Asn Ser Val Glu Thr Glu Asp Phe Gly Met Tyr Phe Cys
            95                  100                 105

caa cag agt aac agc tgg cct ctc acg ttc ggc tcg ggg aca aag ctg      387
Gln Gln Ser Asn Ser Trp Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu
    110                 115                 120

gag atc aaa cgg cgtaagtgtg tcagggtttc acaagaggga ctaaagacat         439
Glu Ile Lys Arg
125
```

gtcagctaat gtgtgactaa tggtaatgtc acttgtcagg atcc   483

<210> 6
<211> 128
<212> PRT
<213> Mus sp.

<400> 6

Met Val Phe Thr Pro Gln Ile Leu Gly Leu Met Leu Phe Trp Ile Ser
1   5   10   15

Ala Ser Arg Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
            20   25   30

Val Thr Pro Gly Asp Ser Val Ser Leu Ser Cys Arg Ala Ser Gln Ile
        35   40   45

Ile Ser Asn Asn Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro
    50   55   60

Arg Leu Leu Ile Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser
65   70   75   80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn
                85   90   95

Ser Val Glu Thr Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Asn
            100   105   110

Ser Trp Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
        115   120   125

<210> 7
<211> 258
<212> DNA
<213> Mus sp.

<220>

<210> misc_feature


```
<221>  misc_feature
<222>  (1)..(258)
<223>  Light chain leader plus sFv of MB3.6


<400>  7
gatatcagat ctcagctgtc tagacatatg gttttcacac ctcagatann nnnnnnnnnn     60

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnngggac aaagctggag    120

atcaaaggtg gctcaggatc gggtggagcc ggctctggtg gctcaggatc ggaagtggtg    180

gtggtggagn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnacc    240

                                                                      258
acggtcaccg tctccagt


<210>  8
<211>  682
<212>  DNA
<213>  Mus sp.

<220>
<221>  CDS
<222>  (20)..(418)
<223>  3D8 Heavy chain V region, plus leader


<400>  8
tgaacacgga cccctcacc atg aac ttc ggg ctc agc ttg att ttc ctt gtc      52
                     Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val
                      1               5                  10

ctt gtt tta aaa ggt gtc cag tgt gaa gtg aag gtg gtg gag tct ggg     100
Leu Val Leu Lys Gly Val Gln Cys Glu Val Lys Val Val Glu Ser Gly
                 15                  20                  25

gga ggc tta gtg aag cct gga gcg tct ctg aaa ctc tcc tgt gca gcc     148
Gly Gly Leu Val Lys Pro Gly Ala Ser Leu Lys Leu Ser Cys Ala Ala
             30                  35                  40

tct gga ttc act ttc agt aac tat ggc atg tct tgg gtt cgc cag act     196
Ser Gly Phe Thr Phe Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Thr
         45                  50                  55

tca gac aag agg ctg gag tgg gtc gca tcc att agt agt ggt ggt gat     244
Ser Asp Lys Arg Leu Glu Trp Val Ala Ser Ile Ser Ser Gly Gly Asp
60                  65                  70                  75
```

```
agc acc ttc tat gca gac aat gta aag ggc cga ttc acc atc tcc aga      292
Ser Thr Phe Tyr Ala Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg
         80                    85                   90

gag aat gcc aag aac acc ctg tac ctg caa atg agt agt ctg aag tct      340
Glu Asn Ala Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser
         95                   100                  105

gag gac acg gcc ttg tat tac tgt gca aga gac gat cta ttt aac tgg      388
Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Asp Asp Leu Phe Asn Trp
        110                  115                  120

ggc caa ggc acc act ctc aca gtc tca tca gccaaaacaa cagccccatc        438
Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
        125                  130

ggtctatcca ctggcccctg tgtgtggaga tacaattggc tcctcggtga ctttaggatg    498

cctggtcaag ggttatttcc ttgagccagt gaccttgacc tggaactctg gatccctgtc    558

cagtggtgtg cacatcttcc cagctgtctt gcagtctgac ctctacaccc tcagcagctc    618

agtgactgta acctcgagca cctggcccag ccagtccatc acttgcaatg tggcccaccc    678

                                                                     682
ggca
```

```
<210>  9
<211>  133
<212>  PRT
<213>  Mus sp.

<400>  9
Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
1             5             10                  15

Val Gln Cys Glu Val Lys Val Val Glu Ser Gly Gly Gly Leu Val Lys
         20                  25                  30

Pro Gly Ala Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
         35                  40                  45

Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Thr Ser Asp Lys Arg Leu
```

```
        50                    55                      60


Glu Trp Val Ala Ser Ile Ser Ser Gly Gly Asp Ser Thr Phe Tyr Ala
65                    70                  75                  80


Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn
                  85                  90                  95


Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu
                100                 105                 110


Tyr Tyr Cys Ala Arg Asp Asp Leu Phe Asn Trp Gly Gln Gly Thr Thr
            115                 120                 125


Leu Thr Val Ser Ser
    130
```

```
<210>  10
<211>  729
<212>  DNA
<213>  Mus sp.

<220>
<221>  CDS
<222>  (15)..(410)
<223>  3D8 Light chain V region, plus leader


<400>  10
ccgttgccgt cgtg atg agt cct gcc cag ttc ctg ttt ctg tta gtg ctc       50
           Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu
            1               5                   10


tgg att cag gaa acc aac ggt gat gtt gta atg acc cag act cca ctc       98
Trp Ile Gln Glu Thr Asn Gly Asp Val Val Met Thr Gln Thr Pro Leu
        15                  20                  25


act ttg tcg gtt acc att gga caa cca gcc tct atc tct tgc aag tca      146
Thr Leu Ser Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser
    30                  35                  40


agt cag agc ctc tta tat agt aat gga aaa acc tat ttg aat tgg tta      194
```

```
Ser Gln Ser Leu Leu Tyr Ser Asn Gly Lys Thr Tyr Leu Asn Trp Leu
45                  50                  55                  60

tta cag agg cca ggc cag tct cca aag cgc cta atc tat ctg gtg tct     242
Leu Gln Arg Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser
                65                  70                  75

aaa ctg gac tct gga gtc cct gac agg ttc act ggc agt gga tca gga     290
Lys Leu Asp Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly
                80                  85                  90

aca gat ttt aca ctg aaa atc agc aga gtg gag gct gag gat ttg gga     338
Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly
            95                  100                 105

gtt tat tac tgc gtg caa ggt aca cat ttt cct cac acg ttc gga ggg     386
Val Tyr Tyr Cys Val Gln Gly Thr His Phe Pro His Thr Phe Gly Gly
        110                 115                 120

ggg acc aag ctg gaa ata aaa cgg gctgatgctg caccaactgt atccatcttc    440
Gly Thr Lys Leu Glu Ile Lys Arg
125                 130

ccaccatcca gtgagcagtt aacatctgga ggtgcctcag tcgtgtgctt cttgaacaac    500

ttctacccca aagacatcaa tgtcaagtgg aagattgatg gcagtgaacg acaaaatggc    560

gtcctgaaca gttggactga tcaggacagc aaagacagca cctacagcat gagcagcacc    620

ctcacgttga ccaaggacga gtatgaacga cataacagct acctgtga ggccactcac      680

aagacatcaa cttcacccat tgtcaagagc ttcaacagga atgagtgtt                729
```

<210> 11
<211> 132
<212> PRT
<213> Mus sp.

<400> 11

```
Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Gln Glu
1               5               10                  15


Thr Asn Gly Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val
            20                  25                  30
```

```
Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu
    35              40              45
```

```
Leu Tyr Ser Asn Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro
    50              55              60
```

```
Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser
65              70              75              80
```

```
Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
            85              90              95
```

```
Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys
        100             105             110
```

```
Val Gln Gly Thr His Phe Pro His Thr Phe Gly Gly Gly Thr Lys Leu
    115             120             125
```

```
Glu Ile Lys Arg
    130
```

```
<210>   12
<211>   736
<212>   DNA
<213>   Mus sp.
```

```
<220>
<221>   CDS
<222>   (14)..(430)
<223>   4D4 Heavy chain V region, plus leader
```

```
<400>   12
actgactcta acc atg gga tgg aga tgg atc ttt ctt ttc ctc ctg tca       49
            Met Gly Trp Arg Trp Ile Phe Leu Phe Leu Leu Ser
            1               5               10
```

```
gga act gca ggt gtc cat tgc cag gtt cag ctg cag cag tct gga cct      97
Gly Thr Ala Gly Val His Cys Gln Val Gln Leu Gln Gln Ser Gly Pro
        15              20              25
```

```
gag ctg gtg aag cct ggg gct tta gtg aag ata tcc tgc aag gct tct        145
Glu Leu Val Lys Pro Gly Ala Leu Val Lys Ile Ser Cys Lys Ala Ser
    30              35                      40

ggt tac acc ttc aca agc tac gat ata aac tgg gtg aag cag agg cct        193
Gly Tyr Thr Phe Thr Ser Tyr Asp Ile Asn Trp Val Lys Gln Arg Pro
45                      50                  55                  60

gga cag gga ctt gag tgg att gga tgg att tat cct gga gat ggt ggt        241
Gly Gln Gly Leu Glu Trp Ile Gly Trp Ile Tyr Pro Gly Asp Gly Gly
                65                  70                  75

act aat tac aat gag aaa ttc aag ggc aag gcc aca ctg act gca gac        289
Thr Asn Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp
                80                  85                  90

aaa tcc tcc agc aca gcc tac atg cag ctc agt agc ctg act tct gag        337
Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu
            95                  100                 105

aac tct gca gtc tat ttc tgt gca aga ggg ggt aac ttc cct tct tat        385
Asn Ser Ala Val Tyr Phe Cys Ala Arg Gly Gly Asn Phe Pro Ser Tyr
    110                 115                 120

gct atg gac tac tgg ggt caa gga acc tca gtc acc gtc tcc tca            430
Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
125                 130                 135

gccaaaacga cacccccatc tgtctatcca ctggcccctg gatctgctgc ccaaactaac      490

tccatggtga ccccgggatg cctggtcaag ggctatttcc ctgagccagt gacagtgacc      550

tggaactctg gatccctgtc cagcggtgtg cacaccttcc cagctgtcct gcagtctgac      610

ctctacactc tgagcagctc agtgactgtc ccctccagca cctggcccag cgagaccgtc      670

acctgcaacg ttgcccaccc ggccagcagc accaaggtgg acaagaaaat tgtgcccagg      730

                                                                       736
gattgt
```

```
<210>   13
<211>   139
<212>   PRT
<213>   Mus sp.

<400>   13
```

Met Gly Trp Arg Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
1   5   10   15

Val His Cys Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
                20   25   30

Pro Gly Ala Leu Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35   40   45

Thr Ser Tyr Asp Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
        50   55   60

Glu Trp Ile Gly Trp Ile Tyr Pro Gly Asp Gly Gly Thr Asn Tyr Asn
65   70   75   80

Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
                85   90   95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asn Ser Ala Val
                100   105   110

Tyr Phe Cys Ala Arg Gly Gly Asn Phe Pro Ser Tyr Ala Met Asp Tyr
        115   120   125

Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
        130   135

<210>   14
<211>   504
<212>   DNA
<213>   Mus sp.

<220>
<221>   CDS
<222>   (7)..(402)
<223>   4D4 Light chain V region, plus leader

<400> 14
```
ctcaaa atg aag ttg cct gtt agg ctg ttg gtg ctg atg ttc tgg att          48
       Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile
       1               5                   10

cct gct tcc aac agt gat gtt ttg atg acc caa tct cca ctc tcc ctg         96
Pro Ala Ser Asn Ser Asp Val Leu Met Thr Gln Ser Pro Leu Ser Leu
15                  20                  25                  30

cct gtc agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag        144
Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
                35                  40                  45

agc att gtc cat agt aat gga gac acc tat tta gaa tgg tac ctg cag        192
Ser Ile Val His Ser Asn Gly Asp Thr Tyr Leu Glu Trp Tyr Leu Gln
            50                  55                  60

aaa cca ggc cag tct cca aag ctc ctg atc tac aag gtt tcc gac cga        240
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asp Arg
        65                  70                  75

ttt tct ggg gtc cca gac agg ttc agt ggc agt gga tca ggg aca gat        288
Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
    80                  85                  90

ttc aca ctc aag atc agc aga gtg gag gct gag gat ctg gga gtt tat        336
Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr
95                  100                 105                 110

ttc tgc ttt caa ggt tca cat gtt ccg tac gcg ttc gga ggg ggg acc        384
Phe Cys Phe Gln Gly Ser His Val Pro Tyr Ala Phe Gly Gly Gly Thr
                115                 120                 125

aag ctg gaa ata aaa cgg gctgatgctg caccaactgt atccatcttc              432
Lys Leu Glu Ile Lys Arg
                130

ccaccatcca gtgagcagtt aacatctgga ggtgcctcag tcgtgtgctt cttgaacaac     492

                                                                      504
ttctacccca aa
```

<210>   15
<211>   132
<212>   PRT
<213>   Mus sp.

<400>   15

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
1   5   10   15

Ser Asn Ser Asp Val Leu Met Thr Gln Ser Pro Leu Ser Leu Pro Val
           20   25   30

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile
           35   40   45

Val His Ser Asn Gly Asp Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro
      50   55   60

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asp Arg Phe Ser
65   70   75   80

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
                85   90   95

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
                100   105   110

Phe Gln Gly Ser His Val Pro Tyr Ala Phe Gly Gly Gly Thr Lys Leu
           115   120   125

Glu Ile Lys Arg
      130

<210>   16
<211>   761
<212>   DNA
<213>   Mus sp.

<220>
<221>   CDS
<222>   (62)..(478)
<223>   3E11 Heavy chain V region, plus leader

```
<400>  16
cctggattca atttccagtt cctcacattc agtgatcagc actgaacacg gacccctcac    60

c atg aac ttc ggg ctc agc ttg att ttc ctt gtc ctt gtt tta aaa ggt   109
  Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
  1               5                  10                  15

gtc cag tgt gaa gtg aaa ctg gtg gag tct ggg gga gac tta atg aac     157
Val Gln Cys Glu Val Lys Leu Val Glu Ser Gly Gly Asp Leu Met Asn
            20                  25                  30

cct gga gcg tct ctg aaa ctc tcc tgt gca gcc tct gga ttc agt ttc     205
Pro Gly Ala Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe
        35                  40                  45

agt aac tat ggc atg tct tgg gtt cgc cag act tca gac aag agg ctg     253
Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Thr Ser Asp Lys Arg Leu
    50                  55                  60

gag tgg gtc gct tcc att agt acg ggt ggt gct aat acc ttc tat cca     301
Glu Trp Val Ala Ser Ile Ser Thr Gly Gly Ala Asn Thr Phe Tyr Pro
65                  70                  75                  80

gac aat gta aag ggc cga ttc acc att tcc aga gag aat gcc aag aac     349
Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn
                85                  90                  95

acc cta tac ctg caa atg agt agt ctg aag tct gag gac acg gcc ttg     397
Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu
            100                 105                 110

tat ttc tgt gca aga gat agt cac tcc gta ggt tgt tgg ttt gct acc     445
Tyr Phe Cys Ala Arg Asp Ser His Ser Val Gly Cys Trp Phe Ala Thr
        115                 120                 125

tgg ggc caa ggg act ctg gtc act gtc tct gca gccaaaacaa cacccccatc    498
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
    130                 135

agtctatcca ctggcccctg ggtgtggaga tactactggt tcctccgtga ctctgggatg   558

cctggtcaag ggctacttcc ctgagtcagt gactgtgact ggaactccg gatccctgcc    618

cagcagtgtg cacaccttcc cagctctcct gcagtctgga ctctacacta tgagcagctc   678

agtgactgtc ccctccagca cctggccaag ccagaccgtt acctgcagtg ttgctcaccc   738

                                                                     761
agccagcagc accacggtgg aca
```

```
<210>  17
<211>  139
<212>  PRT
<213>  Mus sp.

<400>  17
```

Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
1   5   10   15

Val Gln Cys Glu Val Lys Leu Val Glu Ser Gly Gly Asp Leu Met Asn
            20   25   30

Pro Gly Ala Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe
        35   40   45

Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Thr Ser Asp Lys Arg Leu
    50   55   60

Glu Trp Val Ala Ser Ile Ser Thr Gly Gly Ala Asn Thr Phe Tyr Pro
65   70   75   80

Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn
                85   90   95

Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu
            100   105   110

Tyr Phe Cys Ala Arg Asp Ser His Ser Val Gly Cys Trp Phe Ala Thr
        115   120   125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
        130   135

```
<210>  18
<211>  698
<212>  DNA
```

<213> Mus sp.

<220>
<221> CDS
<222> (6)..(401)
<223> 3E11 Light chain V region, plus leader

<400> 18
```
ccagc atg ggc atc aag atg gaa tca cag act ctg gtc ttc ata tcc ata      50
      Met Gly Ile Lys Met Glu Ser Gln Thr Leu Val Phe Ile Ser Ile
      1               5                  10                  15

ctg ctc tgg tta tat gga gct gat ggg aac att gta atg acc caa tct        98
Leu Leu Trp Leu Tyr Gly Ala Asp Gly Asn Ile Val Met Thr Gln Ser
            20                  25                  30

ccc aaa tcc atg tcc atg tca gta gga gag agg gtc acc ttg acc tgc       146
Pro Lys Ser Met Ser Met Ser Val Gly Glu Arg Val Thr Leu Thr Cys
        35                  40                  45

aag gcc agt gag aat gtg gtt act tat gtt tcc tgg tat caa cag aaa       194
Lys Ala Ser Glu Asn Val Val Thr Tyr Val Ser Trp Tyr Gln Gln Lys
        50                  55                  60

cca gag cag tct cct aaa ctg ctg ata tac ggg gca tcc aac cgg tac       242
Pro Glu Gln Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr
    65                  70                  75

act ggg gtc ccc gat cgc ttc aca ggc agt gga tct gca aca gat ttc       290
Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Ala Thr Asp Phe
80                  85                  90                  95

act ctg acc atc agc agt gtg cag gct gaa gac ctt gca gat tat cac       338
Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr His
                100                 105                 110

tgt gga cag ggt tac agc tat ccg tac acg ttc gga ggg ggg acc aag       386
Cys Gly Gln Gly Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys
            115                 120                 125

ctg gaa ata aaa cgg gctgatgctg caccaactgt atccatcttc ccaccatcca       441
Leu Glu Ile Lys Arg
            130

gtgagcagtt aacatctgga ggtgcctcag tcgtgtgctt cttgaacaac ttctacccca     501

aagacatcaa tgtcaagtgg aagattgatg gcagtgaacg acaaaatggc gtcctgaaca     561
```

gttggactga tcaggacagc aaagacagca cctacagcat gagcagcacc ctcacgttga   621

ccaaggacga gtatgaacga cataacagct atacctgtga ggccactcac aagacatcaa   681

                                                                      698

cttcacccat cgtcaag

<210> 19
<211> 132
<212> PRT
<213> Mus sp.

<400> 19

Met Gly Ile Lys Met Glu Ser Gln Thr Leu Val Phe Ile Ser Ile Leu
1   5   10   15

Leu Trp Leu Tyr Gly Ala Asp Gly Asn Ile Val Met Thr Gln Ser Pro
            20   25   30

Lys Ser Met Ser Met Ser Val Gly Glu Arg Val Thr Leu Thr Cys Lys
        35   40   45

Ala Ser Glu Asn Val Val Thr Tyr Val Ser Trp Tyr Gln Gln Lys Pro
    50   55   60

Glu Gln Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr
65   70   75   80

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Ala Thr Asp Phe Thr
                85   90   95

Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys
            100   105   110

Gly Gln Gly Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
            115   120   125

Glu Ile Lys Arg

130